TABLE S4 Fitness score of each gene in the M1 GAS genome after 12 hour saliva incubation.

loous ton	aono nomo	function	Eitness seers*	a value
locus_tag	gene_name	1 111	Fitness score*	q.value
		GTP-binding protein	-0.658984478	0.004613522
M5005_Spy0006		transcription-repair coupling factor	0.152731351	0.022813858
		amino acid permease	-0.244870632	
M5005_Spy0023	M5005_Spy0023	phosphoribosylformylglycinamidine synthase	0.136661559	0.08100213
M5005_Spy0024	purF	amidophosphoribosyltransferase	0.142213903	0.086681958
M5005_Spy0026	purN	phosphoribosylglycinamide formyltransferase	0.231280796	0.056654458
M5005_Spy0027	M5005_Spy0027	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.194261249	0.008249929
M5005 Spy0029		phosphoribosylamineglycine ligase	0.220085098	0.005805314
M5005 Spy0033		adenylosuccinate lyase	0.190920835	0.031026832
M5005 Spy0035	•	holliday junction DNA helicase	-5.355174669	0.001023002
M5005_Spy0033		transcriptional regulator, MarR family	0.326748966	0.088595213
		multimodular transpeptidase-transglycosylase PBP 1B		
M5005_Spy0082		1 1 0, ,	-0.493376495	0.081891422
		adenine-specific methyltransferase	0.169261005	0.016052162
M5005_Spy0096		pyrroline-5-carboxylate reductase	0.182919464	0.081163703
M5005_Spy0097		glutamyl aminopeptidase	0.183742746	0.038729426
M5005_Spy0103	M5005_Spy0103	deoxyadenosine kinase/deoxyguanosine kinase	0.211792279	0.044760874
M5005_Spy0109	M5005_Spy0109	fibronectin-binding protein	0.156437696	0.019843125
M5005_Spy0113	M5005_Spy0113	transposase	0.177952721	0.061179099
M5005 Spy0114	M5005_Spy0114	sortase	0.154083309	0.099426552
		putative DNA-binding protein	0.271197351	0.009825821
M5005_Spy0124		transcriptional regulator	0.185873602	0.013162572
		N-acetylneuraminate-binding protein	0.197142087	0.062727687
M5005_Spy0224		ribulose-phosphate 3-epimerase	-0.69581883	0.016276004
		thiamin pyrophosphokinase	-0.883112446	1.36926E-06
M5005_Spy0238		putative undecaprenol kinase	0.218714424	0.079609375
		undecaprenyl-phosphate alpha-N-acetylglucosaminephosphotransferase	-0.999169025	1.16426E-18
M5005_Spy0241	rgpG	putative cytosolic protein	-0.696209772	3.49051E-10
M5005_Spy0245		iscU protein	-0.315974812	0.08530506
M5005 Spy0246	M5005 Spy0246	ABC transporter-associated protein	-0.217922814	0.094749046
		D-alanyl-D-alanine carboxypeptidase	0.514367681	5.69884E-13
M5005_Spy0249		oligopeptide-binding protein	0.538718209	0.000276915
M5005_Spy0250		oligopeptide transport system permease protein	0.608330115	0.000276016
M5005_Spy0250 M5005_Spy0252				
- ''	• •	oligopeptide transport ATP-binding protein	0.529175008	0.002308473
		iojap protein family	0.250462218	0.035573155
M5005_Spy0288		SWF/SNF family helicase	-0.436535236	1.10495E-07
		aminodeoxychorismate lyase family	-1.398021069	0.008792642
M5005_Spy0297	M5005_Spy0297	transposase	0.187312822	0.090939043
M5005_Spy0308	M5005_Spy0308	putative cytosolic protein	-0.577351766	0.000134024
M5005 Spy0317		putative hemolysin	-0.208183855	0.023585478
M5005_Spy0319		manganese-dependent inorganic pyrophosphatase	-2.077421416	0.000704562
M5005 Spy0339		exodeoxyribonuclease III	-0.510757625	0.000185678
M5005_Spy0362		glucosamine-1-phosphate acetyltransferase/UDP-N-acetylglucosamine pyrophosphorylase	-0.713616392	0.049213846
		putative membrane associated protein	-0.618042214	0.013513682
	M5005_Spy0384		-0.225638512	
		glucosyltransferase	-0.271151013	0.008775124
M5005_Spy0436		two-component sensor histidine kinase	-0.765991318	1.83718E-08
M5005_Spy0439	smc	chromosome partition protein	-0.182969047	0.002909828
M5005_Spy0470	M5005_Spy0470	hydrolase, HAD superfamily	0.144496461	0.099312082
M5005_Spy0486	M5005_Spy0486	hypothetical protein	-0.278131347	0.000105206
M5005 Spy0499	M5005 Spy0499	thiamine transporter	0.582643028	0.002374227
M5005_Spy0516		calcium-transporting ATPase	-1.832712959	0.010438289
M5005 Spy0532		cell division protein	-3.095206603	
		septation ring formation regulator	1.073526865	0.026587383
M5005_Spy0568		streptolysin S export ATP-binding protein	-3.796026607	1.51349E-38
M5005_Spy0569		streptolysin S export transmembrane protein	-3.527444414	1.62459E-32
M5005_Spy0570		streptolysin S export transmembrane protein	-3.385186061	1.63633E-22
		phosphoglycerol transferase	-0.303195648	
		methyltransferase	-0.311312085	
M5005_Spy0624	aroD	3-dehydroquinate dehydratase	-0.893875389	0.006605639
M5005_Spy0628	folC2	folylpolyglutamate synthase/dihydrofolate synthase	0.263048013	0.016342543
M5005_Spy0642		carbamoyl-phosphate synthase small chain	-0.308985613	8.46644E-06
M5005 Spy0643		carbamoyl-phosphate synthase large chain	-0.281185035	3.26425E-08
	M5005 Spy0644		-1.171839609	7.71762E-93
,		ABC transporter ATP-binding protein	-0.907931061	2.42106E-41
			-1.114169732	
		ABC transporter permease protein		5.3171E-92
M5005_Spy0657		thioredoxin reductase	-0.950555933	0.08100213
M5005_Spy0660		fructose repressor	-0.221569848	0.063452252
M5005_Spy0661		1-phosphofructokinase	-0.400752833	0.016577104
M5005_Spy0662	fruA	PTS system, fructose-specific IIABC component	-0.254036683	0.099426552
M5005_Spy0663	mur11	autolysin	-0.180057752	0.053747552
		GTP pyrophosphokinase	-0.188759942	0.095871803
		hypothetical protein	0.284637649	4.69155E-08
		SSU ribosomal protein S1P	1.756768776	0.031196792
M5005_Spy0713 M5005_Spy0728		adenine phosphoribosyltransferase	1.346037774	3.37325E-15
		fibronectin-binding protein	-0.22699608	
M5005_Spy0740		O.		0.016396718
		ABC transporter substrate-binding protein	-0.181541268	0.038801584
		ABC transporter ATP-binding protein	-0.195195149	0.003735527
M5005_Spy0751		pyruvate dehydrogenase E1 component alpha subunit	1.39312003	1.51782E-12
M5005_Spy0752		pyruvate dehydrogenase E1 component beta subunit	1.167556743	1.20726E-05
M5005_Spy0758	lpIB	lipoate-protein ligase A	0.389265511	0.06630619
M5005_Spy0763		phosphoglucosamine mutase	0.380717368	0.070516093
		4-nitrophenylphosphatase	0.233209459	0.03960479
,.	,,			

M5005_Spy0791	uvrC	excinuclease ABC subunit C	-0.174380248	0.016052162
M5005_Spy0817		D-alanyl-D-alanine carboxypeptidase	-0.240331633	
		polysaccharide deacetylase spermidine/putrescine transport system ATP-binding protein	0.180919149	
M5005_Spy0826 M5005_Spy0838	•	lipase/acylhydrolase family protein	-0.605778413 0.277051007	
		GTP pyrophosphokinase	-0.763530261	
M5005_Spy0860		thiamine biosynthesis lipoprotein	-0.618602854	0.08270092
M5005_Spy0864		peptide release factor-glutamine N5-methyltransferase	-0.786814904	
	M5005_Spy0869		-0.521323456	
M5005_Spy0872		NADH oxidase H2O-forming 2-(5"-triphosphoribosyl)-3'-dephosphocoenzyme-A synthase	0.665151436 0.158426349	2.07049E-18 0.061166736
M5005_Spy00906		citrate lyase beta chain/citryl-CoA lyase subunit	0.201673656	0.002822296
M5005_Spy0907		citrate lyase alpha chain/citrate CoA-transferase	0.24846206	0.001334037
M5005_Spy0925		anaerobic ribonucleoside-triphosphate reductase	-0.294058452	
		cardiolipin synthetase	-1.61400844	4.79854E-06
	M5005_Spy0934 M5005_Spy0937	lipoate-protein ligase A	0.174130379 -0.838221881	0.056654458 0.01157833
		nucleoside transport system permease protein	0.720875848	6.61781E-13
		nucleoside transport system permease protein	0.723581053	3.27732E-14
		nucleoside transport ATP-binding protein	0.732785031	9.71289E-16
		nucleoside-binding protein	0.548132533	1.64562E-07
M5005_Spy0943 M5005_Spy0949		cytidine deaminase lysyl aminopeptidase/alanine aminopeptidase	0.555968977 0.152310323	4.60928E-10 0.052092414
M5005_Spy0950		phosphate transport system protein	1.724668039	0.026587383
M5005_Spy0951		phosphate transport ATP-binding protein	-0.570522025	
M5005_Spy0952		phosphate transport ATP-binding protein	-0.710752821	
M5005_Spy0953		phosphate transport system permease protein	-0.719624695	
M5005_Spy0954 M5005_Spy0955		phosphate transport system permease protein phosphate-binding protein	-0.767795237 -0.686473847	
		NAD-dependent K+ or Na+ uptake system component	-1.010507847	
		small integral membrane protein	-0.616659397	
		hypothetical protein	-0.823869594	9.9717E-06
M5005_Spy0987		signal peptidase I	-0.521183455	3.60956E-15
- ''	- ' '	ABC transporter ATP-binding protein ABC transporter permease protein	-1.233018329 -1.482492376	
	M5005_Spy1007		-0.13421468	0.062727687
		terminase large subunit	0.16483824	0.051754079
	M5005_Spy1032		-0.520937834	
	M5005_Spy1044		0.26785544	0.028749554
M5005_Spy1050 M5005_Spy1055		phage transcriptional repressor glycogen phosphorylase	-0.81426741 -0.464464399	0.00104902 2.53003E-20
M5005_Spy1056		4-alpha-glucanotransferase	0.190946321	0.000943514
M5005_Spy1057		transcriptional regulator, Lacl family	0.318576906	6.94701E-06
M5005_Spy1060		maltose transport system permease protein	-0.158650552	
M5005_Spy1066		neopullulanase/cyclomaltodextrinase/maltogenic alpha-amylase	-0.319985153	
M5005_Spy1068 M5005_Spy1070	M5005_Spy1068	protein precursor	-0.283566789 -1.239407079	
M5005_Spy1070		excinuclease ABC subunit B	-0.434689982	
		putative cytosolic protein	0.290339619	3.13717E-05
M5005_Spy1099	M5005_Spy1099	transcriptional regulator, LytR family	-0.252337491	2.79164E-05
M5005_Spy1107		UDP-N-acetylglucosamine 1-carboxyvinyl transferase	-0.718103764	0.03062196
M5005_Spy1108 M5005_Spy1139		S-adenosylmethionine synthetase glucosamine-6-phosphate isomerase	-1.049545437 -0.884123707	
		degV family protein	-0.211590973	
M5005 Spy1229		arginine repressor	-0.310737406	
M5005_Spy1233	M5005_Spy1233	exodeoxyribonuclease VII large subunit	-0.428534745	0.000490899
M5005_Spy1240		ATP-dependent clp protease ATP-binding subunit		2.63157E-08
		putative cytosolic protein ATP-dependent protease La	-1.261136562	3.05751E-07
		arginine/ornithine antiporter	-0.853753259 0.228811713	0.09702059 0.002463814
M5005 Spy1275		arginine deiminase	0.186307456	0.08270092
M5005_Spy1314		hyaluronoglucosaminidase	-0.175893731	0.035015208
		hypothetical protein	-0.399198411	3.79037E-07
		alpha-mannosidase	-0.463215344	6.44134E-11
M5005_Spy1319		tRNA (uracil-5-)-methyltransferase COMF operon protein 3	0.12802925 -0.189249638	0.099877694 0.072289245
		Xaa-Pro dipeptidase	0.193375186	0.057161218
M5005_Spy1333		two-component sensor protein	0.232802719	0.081304282
		D-beta-hydroxybutyrate permease	0.191391351	0.007044961
M5005_Spy1349		autoinducer-2 production protein	0.292587869	0.001995711
M5005_Spy1356 M5005_Spy1375		aminopeptidase C transketolase	0.215706779 -1.805983584	0.00315439 3.53596E-17
M5005_Spy1379		alpha-glycerophosphate oxidase	0.192995821	0.053747552
M5005_Spy1381		glycerol kinase	-0.619046096	1.0811E-11
M5005_Spy1388		N-acetylglucosamine-6-phosphate deacetylase	-0.948841014	2.40063E-21
		hypothetical protein	-0.318840945	0.09702059
		PTS system, galactose-specific IIC component	0.466679867 0.583244158	8.21418E-11 1.16426E-18
		PTS system, galactose-specific IIB component PTS system, galactose-specific IIA component	0.583244158 0.445454846	1.16426E-18 3.82185E-06
M5005_Spy1402		lactose phosphotransferase system repressor	0.258699263	0.000633075
M5005_Spy1421	M5005_Spy1421	phage infection protein	-0.186223164	0.016577104
	M5005_Spy1423	hyaluronoglucosaminidase	-0.196297895	0.027136065
M5005 Spy1424	ME005 0	ninga and and described and	0.00000====	0.070440
M5005 Spy1420		phage endopeptidase	-0.206008503 -0.432535035	0.07644842 2 97587F-17
	M5005_Spy1439		-0.206008503 -0.432535035 -0.393676418	2.97587E-17

M5005_Spy1447 M5005_Spy1447 M5005_Spy1469 0.0256583751 0.037161218 M5005_Spy1452 M5005_Spy1452 M5005_Spy1452 M5005_Spy1462 M5005_Spy1463 M5005_Spy1464 M5005_Spy1469 0.08418066 M5005_Spy1476 M5005_Spy1475 M5005_S					
M5005 Spv1452 M5005 Spv1464 M5005 Spv1464 M5005 Spv1464 M5005 Spv1464 M5005 Spv1464 M5005 Spv1464 M5005 Spv1466 M5005 Spv1466 M5005 Spv1466 M5005 Spv1466 M5005 Spv1466 M5005 Spv1466 M5005 Spv1475 M5005 Spv147				-0.255635751	0.057161218
M5005 Spv1443 M500S, Spv1464 M500S, Spv1464 M500S, Spv1464 M500S, Spv1464 M500S, Spv1464 M500S, Spv1464 M500S, Spv1476 M500S, Spv1477 M500S, Spv1478	M5005_Spy1450	M5005_Spy1450	phage-encoded DNA polymerase	-0.412528601	0.005461935
M5005_Syv146 M5005_Syv146 M5005_Syv1475 4254954762 0.060097375 42227E-07 M5005_Syv1475 0.06073732 42227E-07 M5005_Syv1475 0.06073732 42227E-07 M5005_Syv1475 M5005_Syv1475 M5005_Syv1475 0.06073053 0.060203529 M5005_Syv15716 M5005_Syv15716 M5005_Syv15713	M5005_Spy1452	M5005_Spy1452	phage protein	-0.870685732	0.072289245
M5005_Spy1468 M5005_Spy1476 M5005_Spy1476 M5000S.Spy1476 M5000S.Spy1476 M500S.Spy1476 M50S.Spy1476	M5005_Spy1453	M5005_Spy1453	phage protein	-0.320661979	0.038418056
M5005_Spy1475 M5005_Spy1476 M5005_Spy1475 M5005_Spy1513 M5005_Spy15133 M5005_Spy1513 M5005_Spy1513 M5005_S	M5005_Spy1464	M5005_Spy1464	phage transcriptional regulator, Cro/CI family	-1.254954762	0.006097375
M5005 Spy1613 M5005 Spy1476 M5005 Spy1513 aspartate aminotransferase	M5005_Spy1468	M5005_Spy1468	tRNA (m(7)G46) methyltransferase	-0.667430273	4.42272E-07
M5005 Spy1519 recG	M5005_Spy1475	M5005_Spy1475	acetyltransferase	-0.242288441	0.080203529
M5005, Spy1519 recG AT7-dependent DNA helicase -1.477969971 2.66486-47 M5005, Spy15443 scrR sucrose-cphosphate hydrolase 0.73617578 3.91668E-06 M5005, Spy1566 recD sucrose-cphosphate hydrolase 0.736778937 3.55115E-26 M5005, Spy1566 recD posphatidylgycerophosphatase B -0.34662433 3.85015E-26 M5005, Spy1568 recD codecoxyribonuclease V alpha chain -0.215257523 0.0069737 M5005, Spy1568 recD recomposition of the property	M5005_Spy1476	M5005_Spy1476	ATP/GTP hydrolase	-1.32669054	0.077911829
M5005_Spy1543 scrB	M5005_Spy1513	M5005_Spy1513	aspartate aminotransferase	-0.347847113	4.59772E-08
M5005 Spy1568 Spy1566 M5005 Spy1576 Spy1566 M5005 Spy1569 Spy1566 RecD Spy1566 RecD Spy1566 RecD Spy1569 RecD Spy1569 Spy1576 RecD Spy1576 RecD Spy1576 RecD Spy1576 RecD Spy1576 RecD Spy1577 M5005 Spy1586 RecD Spy1578 Spy1586 RecD Spy1587 Spy1587 RecED Spy1587 Spy158	M5005_Spy1519	recG	ATP-dependent DNA helicase	-1.477959971	2.6649E-47
M5005 Spy1580 M5005 Spy1571 M5005 Spy157	M5005_Spy1543	scrB	sucrose-6-phosphate hydrolase	0.773015774	3.91666E-06
M5005_Spy1566 recD exodeoxyribonuclease V alpha chain -0.215257528 0.006097375 M5005_Spy1576 mupc nucleaside permease 0.21516020 0.001649004 M5005_Spy1586 nupc nucleaside permease 0.161251567 0.028971029 M5005_Spy1586 rupc transcriptional regulator, GntR family -0.283055669 0.038801584 M5005_Spy1617 rupc DNA-directed RNA polymerase deltac chain 0.44260612 1.660022-08 M5005_Spy1681 supc LRNA pseudouridine synthase A -1.410575605 0.000199844 M5005_Spy1682 mmK multiple sugar transport ATP-binding protein -0.200717373 0.056813836 M5005_Spy1687 scl collagen-like surface protein A -0.313629291 0.068166736 M5005_Spy1719 mm1.0 M protein -0.24189316 0.081166736 M5005_Spy1727 mg trans-acting positive regulator -0.45721734 8.75288E-16 M5005_Spy1728 M5005_Spy1728 M5005_Spy17272 M2 Cransporter Permease protein 0.179580566 0.03869871 M5005_Spy1738 <td< td=""><td>M5005_Spy1544</td><td>scrR</td><td>sucrose operon repressor</td><td>0.735678937</td><td>3.55115E-25</td></td<>	M5005_Spy1544	scrR	sucrose operon repressor	0.735678937	3.55115E-25
M5005_Spy1571 M5005_Spy1580 nupC c3-degrading proteinase 0.215180204 0.001649004 M5005_Spy1580 crgR transcriptional regulator, GntR family -0.283055669 0.038801584 M5005_Spy1611 rpoE DNA-directed RNA polymerase delta chain 0.444206192 1.56602E-08 M5005_Spy1637 M5005_Spy1671 ftRNA pseudouridine synthase A 1.41675605 0.00199844 M5005_Spy1638 lacR2 lactose phosphotransferase system repressor 0.313642889 1.95803E-07 M5005_Spy1683 lip luctione rich protein -0.20171373 0.058813636 M5005_Spy1687 sclA collagen-like surface protein A -0.313622291 0.045201594 M5005_Spy1719 emm1. M protein 0.28089771 0.457217364 8.5728BE-16 M5005_Spy1728 rylize mm0. Mprotein 0.280899774 0.0032992 M5005_Spy1727 mga trans-acting positive regulator 0.457217364 8.5728BE-16 M5005_Spy1728 mgb M5005_Spy1728 mgb M5005_Spy1728 mgb 1.5866605 8.5728BE-16 M5005_Spy1727 mga M5005_Spy1728 mgb 1.586050_Spy1728 M5005_Spy1728 mgb 1.5866605 8.5728BE-16	M5005_Spy1560	M5005_Spy1560	phosphatidylglycerophosphatase B	-0.346662463	9.88302E-05
MSD0S_Spy1586 nupC nucleoside permease 0.161251657 0.029871029 MSD0S_Spy1581 rgrR transcriptional regulator, GrIR family -0.283055669 0.038801584 MSD0S_Spy1617 MSD0S_Spy1617 MSD0S_Spy1617 MSD0S_Spy1617 MSD0S_Spy1617 MSD0S_Spy16189 c.0.1410575605 0.000198944 MSD0S_Spy1682 Image of the proper in the permitted of the proper in the permitted in the perm	M5005 Spy1566	recD	exodeoxyribonuclease V alpha chain	-0.215257528	0.006097375
M5005_Spy1689 crgR transcriptional regulator, GnRF family -0.283055669 0.038801584 M5005_Spy1611 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy1617 M5005_Spy16182 M5005_Spy1682 M5005_Spy1782 M5005_Spy1782 M5005_Spy1782 M5005_Spy1782 M5005_Spy1782 M5005_Spy1782 M5005_Spy1784 M5005_	M5005_Spy1571	M5005_Spy1571	c3-degrading proteinase	0.215180204	0.001649004
M5005_Syr1611 rpoE DNA-directed RNA polymerase delta chain 0.444206192 1.56602E-08 M5005_Syr1637 M5005_Syr1637 M5005_Syr1632 IRNA pseudouridine synthase A -1.410575605 0.00199844 M5005_Syr1632 lackse phosphotransferase system repressor 0.313642888 1.95803E-07 M5005_Syr1683 ly leucine rich protein 0-200717373 0.056813636 M5005_Syr1687 sclA collagen-like surface protein A 0-24189316 0.06186736 M5005_Syr179 mm1.0 M protein 0.2808977 0.457217364 0.0628929 M5005_Syr1720 mg ras-acting positive regulator 0.457217364 8.57288E-16 M5005_Syr1726 M5005_Syr1728 M5005_Syr1728 ABC transporter permease protein 0.17988086 0.034511721 0.00035083 M5005_Syr1735 M5005_Syr1737 M5005_Syr1738 M5005_Syr1738 M5005_Syr1738 M5005_Syr1738 M5005_Syr1738 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Syr1739 M5005_Sy	M5005_Spy1586	nupC	nucleoside permease	0.161251567	0.029871029
M5005_Syr1617 M5005_Syr1631 RKNA pseudouridine syrthtase A 1.410575605 0.00199844 M5005_Syr1682 zmmK multiple sugar transport ATP-binding protein 0.200717373 0.056813636 M5005_Syr1683 lrp collagen-like surface protein A -0.24189316 0.061166736 M5005_Syr1780 sch collagen-like surface protein A -0.313629291 0.06249929 M5005_Syr1720 mm1.0 M protein 0.280897974 0.008249929 M5005_Syr1720 mga trans-acting positive regulator 0.457217364 8.57288E-16 M5005_Syr1727 M5005_Syr1727 M5005_Syr1727 ABC transporter permease protein 0.179850868 0.03968931 M5005_Syr1728 M5005_Syr1727 ABC transporter ATP-binding protein 0.28159381 0.304511721 0.00030838 M5005_Syr1737 M5005_Syr1735 psep 1 periplasmic component of efflux system 0.28156622 9.5416622 9.5416622 9.541662 9.001945014 M5005_Syr1737 M5005_Syr1736 M5005_Syr1744 M5005_Syr1744 M5005_Syr1744 M5005_Syr1744 M5005_Syr1744	M5005 Spy1589	crgR	transcriptional regulator, GntR family	-0.283055669	0.038801584
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M5005_Syr1638 lacR2 lactose phosphotransferase system repressor 0.313642889 1.95803E-07 M5005_Syr1683 lrp multiple sugar transport ATP-binding protein -0.20717373 0.0568183636 M5005_Syr1687 sclA collagen-like surface protein A -0.313629291 0.045201594 M5005_Syr1729 mm1.0 M protein 0.280897974 0.0829929 M5005_Syr1726 M5005_Syr1726 M5005_Syr1726 M5005_Syr1726 ABC transporter permease protein 0.179580586 0.039689871 M5005_Syr1728 M5005_Syr1728 ABC transporter ATP-binding protein 0.304511721 0.039698971 M5005_Syr1728 M5005_Syr1728 D4505_Syr1728 D4505_Syr1728 0.039698971 M5005_Syr1728 M5005_Syr1728 D4505_Syr1728 D4505_				-1.410575605	0.000199844
M5005_Spy1683 Irp leucine rich protein -0.24189316 0.061166736 M5005_Spy1687 sclA collagen-like surface protein A -0.313629291 0.45201594 M5005_Spy1720 mga trans-acting positive regulator 0.457217364 8.57288E-16 M5005_Spy1727 M5005_Spy1726 M5005_Spy1727 ABC transporter permease protein 0.304511721 0.000305083 M5005_Spy1728 M5005_Spy1728 M5005_Spy1728 ABC transporter ATP-binding protein 0.304511721 0.000305083 M5005_Spy1736 M5005_Spy1738 periplasmic component of efflux system 0.28159381 2.38165E-05 M5005_Spy1736 M5005_Spy1738 periplasmic component of efflux system 0.51525382 0.007265281 M5005_Spy1737 rgg transcriptional regulator 0.249339696 0.001945019 M5005_Spy1742 M5005_Spy1752 M5005_Spy1754				0.313642889	1.95803E-07
M5005_Spy1683 Irp leucine rich protein -0.24189316 0.061166736 M5005_Spy1687 sclA collagen-like surface protein A -0.313629291 0.45201594 M5005_Spy1720 mga trans-acting positive regulator 0.457217364 8.57288E-16 M5005_Spy1727 M5005_Spy1726 M5005_Spy1727 ABC transporter permease protein 0.304511721 0.000305083 M5005_Spy1728 M5005_Spy1728 M5005_Spy1728 ABC transporter ATP-binding protein 0.304511721 0.000305083 M5005_Spy1736 M5005_Spy1738 periplasmic component of efflux system 0.28159381 2.38165E-05 M5005_Spy1736 M5005_Spy1738 periplasmic component of efflux system 0.51525382 0.007265281 M5005_Spy1737 rgg transcriptional regulator 0.249339696 0.001945019 M5005_Spy1742 M5005_Spy1752 M5005_Spy1754	M5005 Spy1682	msmK	multiple sugar transport ATP-binding protein	-0.200717373	0.056813636
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M5005_Spy1828 M5005_Spy1828 phage infection protein 0.382742226 1.91016E-06 M5005_Spy1830 M5005_Spy1830 K5005_Spy1830 0.221277378 0.02013881 M5005_Spy1837 M5005_Spy1837 phosphoesterase, DHH family protein -1.905262228 1.77982E-21 M5005_Spy1849 M5005_Spy1849 zinc protease 0.311997109 0.001023002 M5005_Spy1850 M5005_Spy1850 zinc protease 0.280126642 0.020213881 M5005_Spy1851 hsA hyaluronan synthase 0.146594367 0.099575179					
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^{*} fitness score is defined as log2 fold changes in sequence read counts between input and output pools. Only genes with statistically significant change (q value < 0.1) are listed.